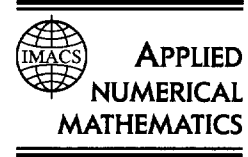




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# Disease transmission models with biased partnership selection<sup>☆</sup>

James M. Hyman<sup>a,\*</sup>, Jia Li<sup>b</sup>

<sup>a</sup> *Theoretical Division, MS-B284, Center for Nonlinear Studies Los Alamos National Laboratory,  
Los Alamos, NM 87545, USA*

<sup>b</sup> *Department of Mathematical Sciences, University of Alabama in Huntsville, Huntsville, AL 35899, USA*

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## Abstract

In multi-group epidemiological models with nonrandom mixing between people in the different groups, often artificial constraints have to be imposed in order to satisfy the balance conditions. We present and analyze simple selective mixing models governed by systems of ordinary differential equations, where the balance conditions are automatically satisfied as a natural consequence of the equations. These models can be applied in situations where biased partnership formations among people in different risk, social, economic, ethnic, or geographic groups must be accounted to accurately predict the epidemic. Because in these models the actual number of partners an individual has depends upon the distribution of the population, the threshold conditions are a sensitive function of this distribution. We formulate threshold conditions for the model and analyze the sensitivity of these conditions to different population distributions, to changes in transmission rates and to the biasing in the partnership selection. These conditions were determined by either explicitly defining a Liapunov function or by using the eigenvalues of the Jacobian matrix to calculate a reproductive number. We present numerical examples to illustrate how the reproductive number depends upon the variations in the population and transmission parameters. Published by Elsevier Science B.V.

**Keywords:** Epidemiological models; Sexually transmitted disease; Selective mixing; Reproductive number

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## 1. Introduction

A major determinant in the spread of sexually transmitted diseases (STDs) is the way that individuals select their sexual partners. It is important to understand and correctly account for the formulation of the partnerships to accurately model an STD epidemic.

Blythe, Busenberg, Castillo-Chavez, and their coworkers [1–4] have formulated multiple group models, where the mixing functions or mixing matrices are based on the average activity,  $c_i$ , of

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\* Corresponding author. E-mail: jh@lanl.gov.

individuals in group  $i$  and the average fraction  $p_{ij}$  of partners in group  $j$  of a person in group  $i$ . Because the partnership formation must satisfy balance constraints to insure that the number of partnerships formed by people in group A with people in group B in a given period of time equals the number of partnerships formed by people in group B with people in group A, often artificial constraints or complicated mathematical derivations must be imposed.

Hyman and Stanley [9,10] formulated risk-based models and pair-formation functions based on the assumption that people in certain groups have priority in choosing their partners. Again, the mixing functions lead to complicated integral equations for the mixing functions, which are mathematically less tractable, and some artificial or special acceptance functions have to be employed.

Jacquez, Koopman, Sattenspiel, Simon, and their coworkers [11–16,18–20] in their sequence of articles introduced heterogeneous mixing in structure models which generate symmetric matrices of the rate of sexual contacts between individuals categorized into discrete population subgroups. Then, the balance constraints are automatically satisfied. This feature simplifies the analysis and numerical approximation of the models, while still accounting for the effects of biased mixing, and provides opportunities in further studies of STDs to take other important factors into consideration [8].

In this article, we analyze a version of the social structured heterogeneous mixing models first proposed by Koopman et al. [14,15], where an individual's preference in the partner selection is predetermined, rather than the number of partners that they have.

We first consider the discrete case where the population is divided into subgroups based on risk levels, age, social behaviors, economic status, ethnic, or geographic positions. We then discuss the basic features of the model in Section 3 and give a mathematical analysis in Section 4 for simple two-group models. A generalization of the model to a continuum is given in Section 5 and our findings are summarized in Section 6.

## 2. The biased preference model formulation

We divide the susceptible and infected populations into  $K$  groups,  $S_i$  and  $I_i$ ,  $i = 1, \dots, K$ , according to their risk level or other factors, and consider the following simple SI model with constant recruitment rate,

$$\begin{cases} \frac{dS_i}{dt} = \mu(S_i^0 - S_i) - \lambda_i S_i, \\ \frac{dI_i}{dt} = -(\mu + \nu_i)I_i + \lambda_i S_i, \end{cases} \quad i = 1, \dots, K, \quad (2.1)$$

where  $\mu$  is the natural death rate,  $1/\nu_i$  is the mean duration of the incubation period,  $\lambda_i$  is the rate of infection, and  $\mu S_i^0$  is the rate of recruitment into group  $i$ .

The formation of partnerships plays an essential role in determining the functional  $\lambda_i$ . We define a partnership to be sexual activity between two people where the infection can be transmitted (e.g., sexual intercourse). We assume people in each group behave the same when selecting a partner, but have biases between groups. In other words, mixing within each group is assumed to be homogeneous but there is heterogeneous mixing among the groups. The formation of partnerships is one of the most important factors in modeling STDs. It depends on the desirability of an active individual, the acceptability of his/her potential partners, and the availability of these potential partners.

Let  $q_{ij}$  be the preference of people in group  $i$  to have a partner from group  $j$ ; that is,  $q_{ij}$  is the fraction of people in group  $j$  with whom an individual in group  $i$  desires forming a partnership. Thus  $q_{ij}$  describes the desirability of people in group  $i$  to have a partner from group  $j$ . It is also the acceptability of people in group  $j$  to people in group  $i$ .

Under the condition that enough potential partners are available, the probability  $p_{ij}$  that a partnership forms between individuals from group  $i$  and group  $j$ , or the mutually acceptable rate for sex, see [14], is

$$p_{ij} := q_{ij}q_{ji}. \quad (2.2)$$

Define  $c_i$  to be the number of social contacts for a person in group  $i$ . The probability that a contact is with a person from group  $j$  is  $c_j N_j / \sum_k c_k N_k$ , where  $N_k = S_k + I_k$ . This also characterizes the availability of contacts with partners in group  $j$ . Hence, the probability of a partnership forming between individuals from group  $i$  and group  $j$  is  $p_{ij} c_j N_j / \sum_k c_k N_k$ .

We define  $\beta_{ij}$  to be the probability of disease transmission per sexual contact between an infected partner in group  $j$  and a susceptible individual in group  $i$ . Under these assumptions, the infection rate of people in group  $i$  is

$$\lambda_i = c_i \sum_{j=1}^K p_{ij} \beta_{ij} \frac{c_j I_j}{\sum_k c_k N_k}. \quad (2.3)$$

The preferences need not be symmetric (i.e.,  $q_{ij} \neq q_{ji}$ , when  $i \neq j$ ), but the probability of a partnership forming is symmetric since  $p_{ij} = q_{ij}q_{ji}$  implies  $p_{ij} = p_{ji}$ . Also, we note that there is no constraint on  $\sum_j q_{ij}$ , which may be less than or greater than one.

Two special cases of the model (2.1) with the infection rate (2.3) are the restricted mixing model when  $q_{ij} = 0$  (hence  $p_{ij} = 0$ ,  $i \neq j$ ) and the proportional mixing model when  $q_{ij} \equiv 1$ , for  $i, j = 1, \dots, K$  [11].

### 2.1. Balance constraints

We denote the number of contacts per unit time of people in group  $i$  with people in group  $j$  by  $T_{ij}$ . The number of contacts with people in group  $i$  that people in group  $j$  have is also  $T_{ij}$ , that is  $T_{ij} = T_{ji}$ . These are the balance constraints that need to be satisfied at all times. In multi-group models where an attempt is made to directly control the number of partnerships formed between groups, these balance conditions usually are artificially enforced (see, e.g., [9–12,17]). However, in the selective mixing model, the balance constraint

$$T_{ij} = p_{ij} \frac{c_j N_j}{\sum_k c_k N_k} c_i N_i = p_{ji} \frac{c_i N_i}{\sum_k c_k N_k} c_j N_j = T_{ji} \quad (2.4)$$

is automatically satisfied. Thus, by using the acceptability  $q_{ij}$  or desirability  $q_{ji}$  of an individual from group  $i$  to an individual from group  $j$  as the primary control variable in these models (instead of the number of partners an individual from group  $i$  desires from group  $j$ ), the balance constraints become a natural consequence of the model, rather than an artificially imposed constraint.

## 2.2. The actual number of contacts

The number of sexual contacts per individual per unit time in many multi-group models is assumed to be constant. When all  $q_{ij}$ 's equal one (proportional mixing), this is also true for the selective mixing model. However, if the mixing is biased, the actual number of contacts, denoted by  $r_i$ , for the selective mixing model will vary in time depending on the combination of desirability, acceptability, and availability.

Define  $P(i)$  as the probability that an individual in group  $i$  finds a partner from any group. The actual number of contacts per person in group  $i$ ,

$$r_i = c_i P(i) = c_i \left( \sum_{j=1}^K p_{ij} \frac{c_j N_j}{\sum_k c_k N_k} \right), \quad (2.5)$$

reaches its maximum  $c_i$  only for the proportional mixing, where  $p_{ij} \equiv 1$  (i.e., everyone is acceptable as a partner).

If the mixing is biased, the acceptability and the availability of partners must be taken into consideration and a limitation may occur. Then  $p_{ij} \leq 1$ , and hence  $r_i \leq c_i$ .

**Example 1.** Consider the two-group model governed by

$$\begin{cases} \frac{dS_i}{dt} = \mu(S_i^0 - S_i) - \lambda_i S_i, \\ \frac{dI_i}{dt} = -(\mu + \nu_i)I_i + \lambda_i S_i, \end{cases} \quad i = 1, 2, \quad (2.6)$$

with

$$\lambda_i = \frac{c}{N} (p_{i1}\beta_{i1}I_1 + p_{i2}\beta_{i2}I_2).$$

Here, for simplicity, we assume that the number of social contacts in both groups are the same:  $c_i \equiv c$ . The actual number of contacts is  $r_i = (c/N)(p_{i1}N_1 + p_{i2}N_2)$  and

$$r_1 - r_2 = \frac{c}{N} ((p_{11} - p)N_1 + (p - p_{22})N_2),$$

where  $p := p_{12} = p_{21}$  and  $N := N_1 + N_2$ .

If  $p_{11} < p < p_{22}$ , the mutually acceptable rate of sex for people in group 1 with people in group 2 is greater than that with their own group, but people in group 2 have higher mutually acceptable rate of sex with their own group. Hence  $r_1 < r_2$ ; that is, the probability of forming a partnership for people in group 1 is less than that for people in group 2. On the other hand, if  $p_{11} < p$  and  $p > p_{22}$ , people in both group attempt to form partnerships with people in other group. In this case, the availability of potential partners will play a more important role. We use the following model parameters to demonstrate the observation:

$$\begin{aligned} S_1^0 &= 350, & S_1(0) &= 350, & I_1(0) &= 10, & S_2^0 &= 100, & S_2(0) &= 100, & I_2(0) &= 250, \\ \nu_1 &= 0.15, & \nu_2 &= 0.15, & q_{11} &= 0.6, & q_{12} &= 1, & q_{21} &= 0.5, & q_{22} &= 0.2, \\ \mu &= 0.015, & c &= 5, & \beta_{ij} &= 0.1. \end{aligned}$$

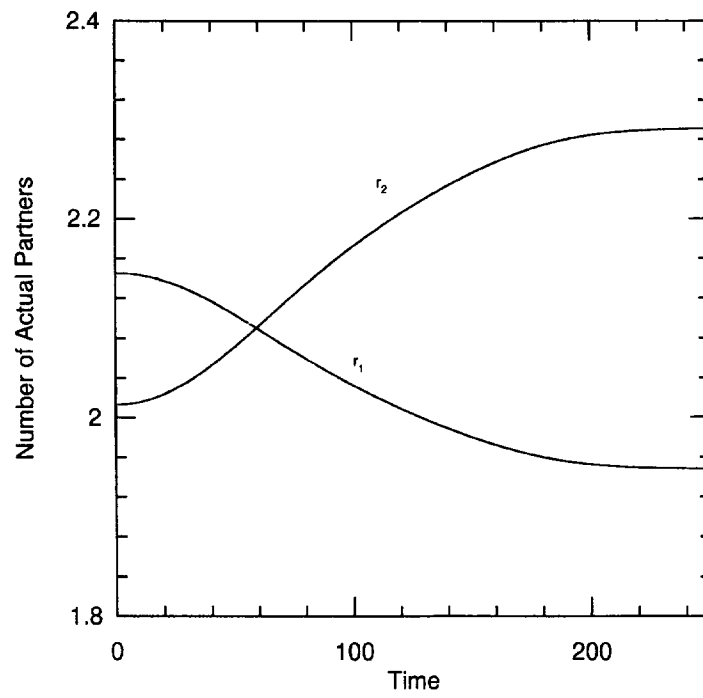


Fig. 1.

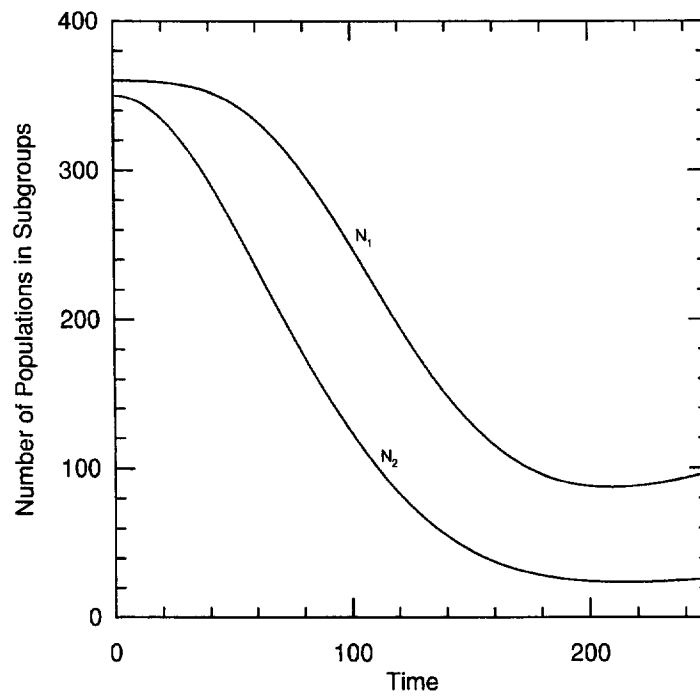


Fig. 2.

The actual numbers of contacts for people in group 1 and group 2 as functions of time are illustrated in Fig. 1 and the numbers of populations in the subgroups are illustrated in Fig. 2.

Since  $p_{11} = q_{11}^2 = 0.36$ ,  $p_{22} = q_{22}^2 = 0.3$ , and  $p = q_{12}q_{21} = 0.5$ , people in both groups prefer their partners from the other group. In the beginning,  $N_1$  and  $N_2$  are close. Because  $p_{11} > p_{22}$ , the number of actual contacts of people in group 1 is greater than that of people in group 2. However, as time elapses, the population size in group 2,  $N_2$ , is much smaller than that in group 1,  $N_1$ . People in group 2, who attempt to find partners in group 1, have more chances to succeed than people in group 1, who attempt to find partners in group 2.

### 3. Preliminary studies

#### 3.1. Thresholds

The concept of threshold conditions is one of the most important concepts in mathematical epidemiology (see [6,7,13,21]). It specifies when the disease will spread if a small number of infected people are introduced into the susceptible population. The threshold conditions are usually characterized by the reproductive number which is determined by the stability of the infection-free equilibrium.

In model (2.1), the stability of the infection-free equilibrium ( $S_i = S_i^0$ ,  $I_i = 0$ ),  $i = 1, \dots, K$ , is completely determined by the equations for  $I_i$ , and can be investigated by either constructing a Liapunov function or locating the eigenvalues of the Jacobian matrix evaluated at the equilibrium.

Assume that the transmission probability  $\beta_{ij} = \xi_i \zeta_j$  is the product of the susceptibility of the uninfected person in group  $i$ ,  $\xi_i$ , and the infectiousness of the infected individual in group  $j$ ,  $\zeta_j$ . Suppose that people select their partners without discrimination of groups so that  $q_{ij} = q_i$  and hence  $p_{ij} = q_i q_j$ . Then we can use the Liapunov function motivated from [20],

$$V = \sum_j \frac{\zeta_j q_j c_j I_j}{\mu + \nu_j}.$$

When the total time derivative of  $V$  along solutions of model (2.1),

$$\begin{aligned} \dot{V} &= \frac{1}{N^0} \sum_j \frac{S_j^0 \xi_j \zeta_j q_j^2 c_j^2}{\mu + \nu_j} \sum_k \zeta_k q_k c_k I_k - \sum_j \zeta_j q_j c_j I_j \\ &= \left( \frac{1}{N^0} \sum_j \frac{S_j^0 \xi_j \zeta_j q_j^2 c_j^2}{\mu + \nu_j} - 1 \right) \sum_j \zeta_j q_j c_j I_j, \end{aligned}$$

is positive, the epidemic grows. Here  $N^0 = \sum_{i=1}^K c_i S_i^0$ . This determines the reproductive number

$$R_0 = \frac{1}{N^0} \sum_j \frac{S_j^0 \xi_j \zeta_j q_j^2 c_j^2}{\mu + \nu_j}.$$

In the more general case when  $p_{ij} \neq q_i q_j$ , we can use the Liapunov function

$$V = \sum_j \left( \sum_i \beta_{ij} p_{ij} \right) \frac{c_j I_j}{\mu + \nu_j}.$$

Its time total derivative is

$$\begin{aligned}\dot{V} &= - \sum_j \sum_i \beta_{ij} p_{ij} c_j I_j + \sum_j \left( \sum_i \beta_{ij} p_{ij} \right) \frac{c_j^2 S_j^0}{(\mu + \nu_j) N^0} \sum_k \beta_{jk} p_{jk} c_k I_k \\ &= \sum_j \left( \left( \frac{c_j^2 S_j^0}{(\mu + \nu_j) N^0} \sum_i \beta_{ij} p_{ij} \right) - 1 \right) \sum_k \beta_{jk} p_{jk} c_k I_k.\end{aligned}$$

Then, we can define the reproductive number for the  $i$ th subgroup as

$$R_{i0} = \frac{c_i^2 S_i^0}{(\mu + \nu_i) N^0} \left( \sum_j \beta_{ji} p_{ji} \right).$$

If  $R_{i0} > 1$ , for all  $i$ , the epidemic persists in the population. If  $R_{i0} < 1$ , for all  $i$ , the disease-free equilibrium is globally asymptotically stable and the epidemic dies out in the population, regardless of the initial levels of infection.

A more interesting case occurs when there are  $R_{i0}$ 's both greater than and less than one. In this case, it is difficult to construct a suitable Liapunov function to determine a reproductive number for the whole population. Then, we can derive reproductive numbers by investigating local stability of the infection-free equilibrium, that is, the location of eigenvalues of the following Jacobian matrix:

$$J = \begin{pmatrix} -\mu - \nu_1 + \frac{\beta_{11} p_{11} S_1^0 c_1}{N^0} & \frac{\beta_{12} p_{12} S_1^0 c_2}{N^0} & \cdots & \frac{\beta_{1K} p_{1K} S_1^0 c_K}{N^0} \\ \frac{\beta_{21} p_{21} S_2^0 c_1}{N^0} & -\mu - \nu_2 + \frac{\beta_{22} p_{22} S_2^0 c_2}{N^0} & \cdots & \frac{\beta_{2K} p_{2K} S_2^0 c_K}{N^0} \\ \vdots & \vdots & \ddots & \vdots \\ \frac{\beta_{K1} p_{K1} S_K^0 c_1}{N^0} & \frac{\beta_{K2} p_{K2} S_K^0 c_2}{N^0} & \cdots & -\mu - \nu_K + \frac{\beta_{KK} p_{KK} S_K^0 c_K}{N^0} \end{pmatrix}$$

(see, e.g., [5–7]).

In general, it is not an easy task to locate the eigenvalues of the Jacobian matrix. However, the eigenvalues of the Jacobian for the two-group model can be calculated explicitly and the reproductive number for the whole population can be represented by

$$R_0 = \frac{1}{(2\mu + \nu_1 + \nu_2) N^0} \left( \alpha_{11} + \alpha_{22} + \sqrt{(\nu_1 - \nu_2 + \alpha_{22} - \alpha_{11})^2 + 4\alpha_{12}\alpha_{21}} \right), \quad (3.1)$$

where

$$\begin{aligned}\alpha_{11} &= S_1^0 c_1^2 \beta_{11} p_{11}, & \alpha_{12} &= S_1^0 c_1 c_2 \beta_{12} p_{12}, \\ \alpha_{21} &= S_2^0 c_1 c_2 \beta_{21} p_{21}, & \alpha_{22} &= S_2^0 c_2^2 \beta_{22} p_{22}.\end{aligned}$$

In fact, in this case, the Jacobian has the following form:

$$J = \begin{pmatrix} -\mu - \nu_1 + \frac{\beta_{11} p_{11} S_1^0 c_1^2}{N^0} & \frac{\beta_{12} p_{12} S_1^0 c_1 c_2}{N^0} \\ \frac{\beta_{21} p_{21} S_2^0 c_1 c_2}{N^0} & -\mu - \nu_2 + \frac{\beta_{22} p_{22} S_2^0 c_2^2}{N^0} \end{pmatrix}.$$

Denote  $\delta_i = \mu + \nu_i$ , and  $a_{ij} := \beta_{ij} p_{ij} S_i^0 c_i c_j / N^0$ ,  $i, j = 1, 2$ . Then

$$\mathbf{J} = \begin{pmatrix} -\delta_1 + a_{11} & a_{12} \\ a_{21} & -\delta_2 + a_{22} \end{pmatrix}. \quad (3.2)$$

The eigenvalues of (3.2) are

$$\rho = \frac{1}{2} \left( -(\delta_1 - a_{11} + \delta_2 - a_{22}) \pm \sqrt{((\delta_1 - a_{11}) - (\delta_2 - a_{22}))^2 + 4a_{12}a_{21}} \right).$$

Since  $((\delta_1 - a_{11}) - (\delta_2 - a_{22}))^2 + 4a_{12}a_{21} > 0$ , the larger eigenvalue is

$$\rho^* := \frac{1}{2} \left( -(\delta_1 - a_{11} + \delta_2 - a_{22}) + \sqrt{((\delta_1 - a_{11}) - (\delta_2 - a_{22}))^2 + 4a_{12}a_{21}} \right).$$

Hence, (3.2) is stable if  $\rho^* < 0$ , or equivalently,

$$a_{11} + a_{22} + \sqrt{((\delta_1 - a_{11}) - (\delta_2 - a_{22}))^2 + 4a_{12}a_{21}} < \delta_1 + \delta_2,$$

and (3.2) is unstable if

$$a_{11} + a_{22} + \sqrt{((\delta_1 - a_{11}) - (\delta_2 - a_{22}))^2 + 4a_{12}a_{21}} > \delta_1 + \delta_2.$$

Then, the reproductive number in (3.1) is obtained.

### 3.2. Sensitivity of the reproductive number

The reproductive number combines all the demographic and epidemiological parameters and the complex dynamics of the disease transmission is sensitive to combinations of these parameters. To gain insight into this sensitivity, we now analyze the effects of parameter changes on the reproductive number. First, the reproductive number  $R_0$  in (3.1) increases if the transmission rate  $\beta_{ij}$ , the mean duration of the incubation period  $1/\nu_i$ , the number of the social contacts  $c_i$ , the probability of partnership formation  $p_{ij}$ , or recruitment rate  $S_i^0$  increases, which is determined by the positive growth rates

$$\frac{\partial R_0}{\partial \beta_{ij}}, \quad \frac{\partial R_0}{\partial (1/\nu_i)}, \quad \frac{\partial R_0}{\partial c_i}, \quad \frac{\partial R_0}{\partial p_{ij}}, \quad \frac{\partial R_0}{\partial S_i^0}.$$

Next, for simplicity, we assume that the transmission probability  $\beta_{ij}$  and the mean duration of the incubation period,  $1/\nu_i$ , are independent of groups, that is,  $\beta_{ij} \equiv \beta$ ,  $c_i \equiv c$ , and  $\nu_i \equiv \nu$ . Then, the reproductive number becomes

$$R_0 = \frac{\beta c^2}{2(\mu + \nu)N^0} \left( p_{11}S_1^0 + p_{22}S_2^0 + \sqrt{(p_{11}S_1^0 - p_{22}S_2^0)^2 + 4p_{12}p_{21}S_1^0S_2^0} \right).$$

The sexual behavior of individuals is characterized by  $q_{ij}$ . For people in group  $i$ , the larger  $\sum_j q_{ij}$  is, the fewer selective they are about whom they form a partnership with. Consider the case where the behavior of people in group 2,  $(q_{21}, q_{22})$ , and the average desirability of people in group 1,  $Q := q_{11} + q_{12}$ , are fixed. That is, we assume people in group 1 may switch their preference between the two groups, but their “total” preference does not change. We now use  $q_{12} := q$ ,  $0 \leq q \leq Q$ , as a parameter to study the effects of the relative desirability of people in group 2 on the reproductive



number. A large  $q$  implies that people in group 1 prefer their partners more from group 2 and are less interested in forming partners within their own group.

In terms of  $q$ ,

$$R_0(q) = \frac{c\beta}{2(\mu + \nu)N} \left( (Q - q)^2 S_1^0 + q_{22}^2 S_2^0 + \sqrt{((Q - q)^2 S_1^0 - q_{22}^2 S_2^0)^2 + 4q_{21}^2 S_1^0 S_2^0} \right).$$

A straightforward calculation shows that if

$$S_1^0 Q^2 \leq q_{22}^2 S_2^0,$$

the reproductive number  $R_0(q)$  is an increasing function of  $q$ . If

$$S_1^0 Q^2 > q_{22}^2 S_2^0,$$

there exists a unique  $q^*$ , in  $(0, Q)$ , such that the reproductive number  $R_0(q)$  assumes its minimum at  $q^*$ .  $R_0(q)$  decreases as  $q$  increases from 0 to  $q^*$  and increases as  $q$  increases from  $q^*$  to  $Q$ . When  $S_1^0 \leq q_{22}^2 S_2^0 / Q^2$ ,  $S_1^0 Q^2 \leq q_{22}^2 S_2^0$ . Partners will be more likely formed with people in group 2. Then, as the preference with people in group 2 for people in group 1 increases, more partnerships will be formed and the infection spreads faster. On the other hand, if  $S_1^0 > q_{22}^2 S_2^0 / Q^2$ , that is  $S_1^0 Q^2 > q_{22}^2 S_2^0$ , the probability of partnership formation within group 2 is smaller than the probability of partnership formation of people in group 1. As people in group 1 increase their preference with people in group 2 to  $q^*$ , they decrease their preference within their own group since  $q_{12} + q$  is constant. Then, less partnerships will be formed and the infection spreads slower. However, if  $q$  exceeds  $q^*$ , the probability of partnership formation for people in group 2 with people in group 1,  $p_{21} = q_{21}q$ , increases and more partnerships are formed, which leads to an increase of  $R_0$  again. For small  $q_{22}$  and  $q$  ( $\leq q^*$ ), most partnerships are formed within group 1. As  $q$  increases,  $Q - q$  decreases. Then there are fewer partnerships formed, and  $R_0$  decreases. When  $q$  exceeds  $q^*$ , most partnerships are not formed within group 1, but between group 1 and group 2, and  $R_0$  increases. If  $q_{22}$  is large, an increase in  $q$  will cause more partnerships to form which leads to  $R_0$  always increasing as  $q$  increases. These relationships are illustrated in the following example.

**Example 2.** Consider model (2.6) again with the parameters

$$\begin{aligned} S_1^0 &= 100, & S_2^0 &= 200, & \beta &= 0.15, & \mu &= 0.015, & \nu &= 0.15, & c &= 5, \\ q_{21} &= 0.5, & Q &= 1, \end{aligned}$$

where we increase  $q_{22}$  from 0.3 to 0.7 with an increment 0.05. The reproductive number is an increasing function of  $q$  when  $q_{22} \geq 0.7$ , since  $S_1^0 Q^2 \leq q_{22}^2 S_2^0$ . When  $q_{22} < 0.7$ ,  $S_1^0 Q^2 > q_{22}^2 S_2^0$ , and the reproductive number as a function of  $q$  is concave and the smaller  $q_{22}$  is, the larger the minimum point  $q^*$  is. The reproductive numbers, as functions of  $q$ , for different  $q_{22}$  are illustrated in Fig. 3.

The numbers of susceptibles and infectives with  $q_{22} = 0.3$  are shown in Fig. 4, where  $q = q_{12} = 0.3$ , and in Fig. 5, where  $q = q_{12} = 0.9$ , respectively. As is shown in Fig. 3, there is a threshold value of  $q$  such that  $R_0$  changes from decrease to increase. When  $q = q_{12} = 0.3$ , the reproductive number is less than one and hence the epidemic dies out. When  $q = q_{12} = 0.9$ ,  $R_0 > 1$ . The epidemic persists in the population.

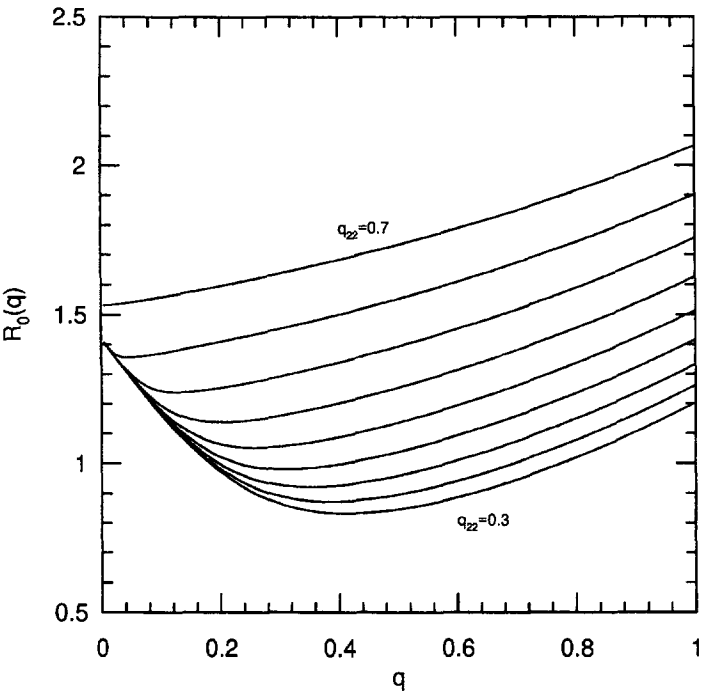


Fig. 3.

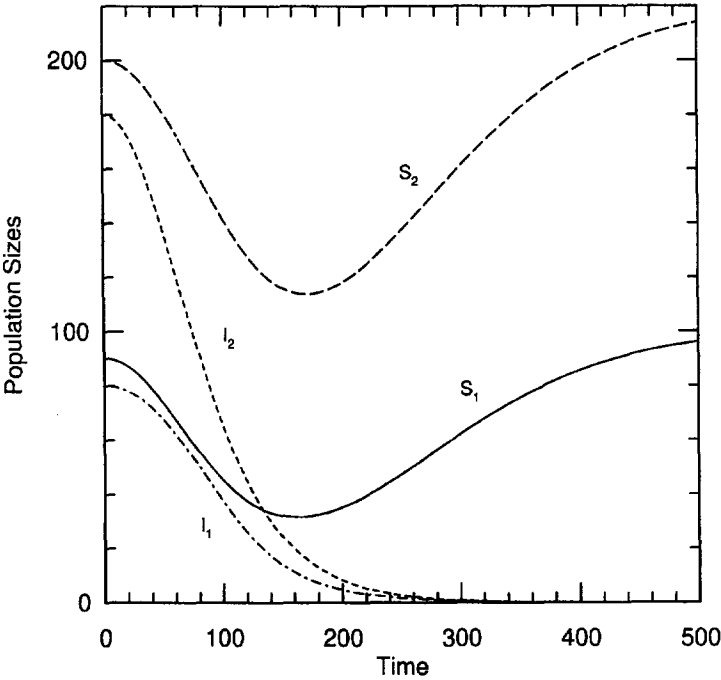


Fig. 4.

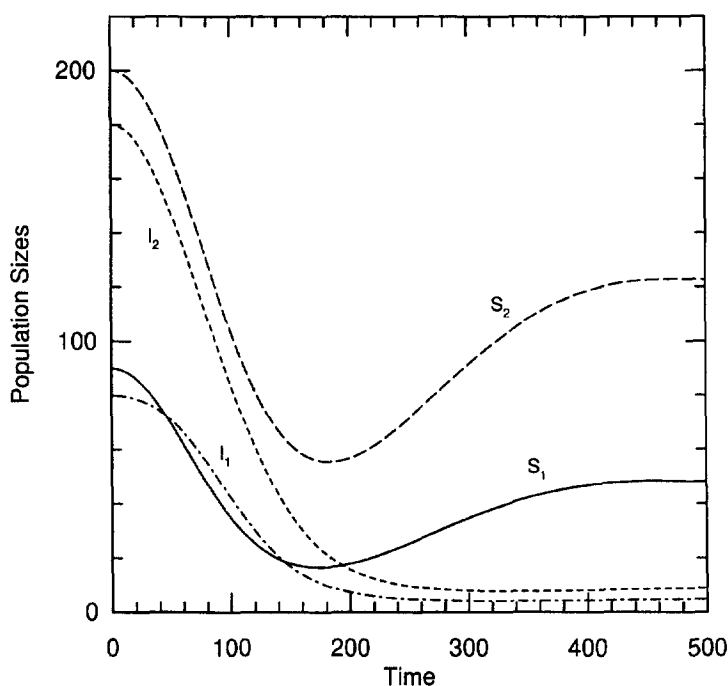


Fig. 5.

#### 4. Generalization to a continuum

The selective mixing model can also be applied to a population with a continuum of biased mixing behavior.

Let  $x$  be a continuous state vector of characteristics (such as age, geographical positions, or behavioral traits) of individuals in a population  $X$ . Let  $S(t, x)$  and  $I(t, x)$  be the continuous densities of the susceptible and infected subpopulations respectively and define  $N(t, x) := S(t, x) + I(t, x)$ .

Assume that the desirability of an individual in state  $x$  to form a partnership with an individual in state  $y$  is described by  $q(x, y)$ ,  $x, y \in X$ . The acceptability of an individual of state  $x$  to an individual of state  $y$  then is  $q(y, x)$ .

Define  $c(x)$  as the number of social contacts of an individual in state  $x$ . The availability of individuals with state  $y$  in the population is  $c(y)N(t, y)/W(t)$ , where  $W(t) := \int_{x \in X} c(x)N(t, x) dx$ , and the actual number of contacts of an individual of state  $x$  per unit time is

$$r(t, x) = \frac{1}{W(t)} \int_{y \in X} q(x, y)q(y, x)c(y)N(t, y) dy.$$

The infection rate of a susceptible individual in state  $x$  by an infected individual in state  $y$  can be expressed as

$$\lambda(t, x) = \frac{1}{W(t)} \int_{y \in X} \beta(x, y)q(x, y)q(y, x)c(y)I(t, y) dy,$$

where  $\beta(x, y)$  is the transmission rate of the disease from an infected individual in state  $y$  to a susceptible individual in state  $x$ .

The probability that a partnership forms,  $p(x, y) := q(x, y)q(y, x)$ , is symmetric and the balance constraints are automatically satisfied.

The dynamics of the epidemic is governed by the following system:

$$\begin{aligned} D_t S(t, x) &= \Lambda(x) - (\mu(x) + \lambda(t, x))S(t, x), \\ D_t I(t, x) &= \lambda(t, x) - (\mu(x) + \nu(x))I(t, x), \end{aligned}$$

where  $D_t$  denotes the total derivative with respect to time and  $\Lambda(x)$  is the flow into the susceptible population.

There is an infection-free equilibrium  $(S^0(x), 0)$ , where  $S^0(x)$  can be explicitly solved from

$$\frac{dS(x)}{dx} = \Lambda(x) - \mu(x)S(x).$$

The stability of this infection-free equilibrium defines the threshold conditions for the continuous model similar to those analyzed for the discrete model in Section 3. We plan our investigations into the dynamics of this model and will describe them in a near future.

## 5. Discussion

We start with the preference behaviors of individuals in the sexually active population to formulate a variation of the selective mixing model proposed in [14]. One of the main features of the selective mixing model is that the balance constraints for biased mixing functions are automatically satisfied. The approach can be applied to situations such as mixing between people in different social, economic, ethnic, or geographic groups, where biased partnership formation is central and where the satisfaction of the balance conditions may be extremely complex.

Another important feature of the selective mixing model is that the partnerships formed in the population depend on the desirability and acceptability of individuals in each group. While the number of social contacts of people in each group is presumed, the actual number of partnerships formed depend upon the number of potential partners available and initial acceptance. We believe that in many situations this is a more reasonable assumption than the fixed number of partners in each group independent of the availability of desirable partners. Moreover, this important feature results in more flexible models for nonrandom mixing including other factors for the spread of the disease as is discussed in [9,10], and models taking other important factors such as density dependence into consideration [8].

For mathematical simplicity, we assume that the desirability and the acceptability are constant in the model. This implies that the acceptability of partners is independent of the environment. This simplification allows us to formulate explicit threshold conditions for the model and analyze the sensitivity of these conditions to changes in transmission rates and to the biasing in the partnership selection. The threshold conditions are a sensitive function of the distribution of the population among the different groups. The explicit representation of the threshold conditions clearly illustrate how changes in the population could dramatically affect the reproductive number of the epidemic. The simplification of the model does however restrict its applicability in a rapidly changing population.

In a more realistic model, people would adjust their acceptability according to availability of their desired partners. That is, the acceptabilities  $q_{ij}$  should be density dependent functionals of  $N_i$  or  $I_i/N_i$ , although this modification certainly increases difficulty in mathematical analysis (see [8]).

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